```
  1  CAGTGTGCTG GCGGCCCGGC GCGAGCCGGC CCGGCCCCGG TCGGGCCTCC
-26

     GAAACC   ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC
                M   N   F   L   L   S   W   V   H   W   S
              -26                         -20

 90  CTC GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG
-15  L   A   L   L   L   Y   L   H   H   A   K   W   S   Q
                            -10

     GCT|GCA CCC ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC
     A  |A   P   M   A   E   G   G   G   Q   N   H   H
     -1 +1                +5                  +10

171  GAA GTG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC TAC TGC
 13  E   V   V   K   F   M   D   V   Y   Q   R   S   Y   C
       +15                     +20                     +25

     CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC
     H   P   I   E   T   L   V   D   I   F   Q   E   Y
               +30                 +35

252  CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC
 40  P   D   E   I   E   Y   I   F   K   P   S   C   V   P
   +40                 +45                 +50

     CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG
     L   M   R   C   G   G   C   C   N   D   E   G   L
       +55                 +60                 +65

333  GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT
 67  E   C   V   P   T   E   E   S   N   I   T   M   Q   I
               +70                 +75                 +80

     ATG CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG
     M   R   I   K   P   H   Q   G   Q   H   I   G   E
                   +85                 +90

414  ATG AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC AGA CCA AAG
 94  M   S   F   L   Q   H   N   K   C   E   C   R   P   K
       +95                 +100                +105

     AAA GAT AGA GCA AGA CAA GAA AAT CCC TGT GGG CCT TGC
     K   D   R   A   R   Q   E   N   P   C   G   P   C
           +110                +115                +120

495  TCA GAG CGG AGA AAG CAT TTG TTT GTA CAA GAT CCG CAG ACG
121  S   E   R   R   K   H   L   F   V   Q   D   P   Q   T
                 +125                +130

     TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC AAG
     C   K   C   S   C   K   N   T   D   S   R   C   K
   +135                +140                +145
```

FIG. 1A

```
576  GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AGA TGT GAC
148  A   R   Q   L   E   L   N   E   R   T   C   R   C   D
         +150                    +155                +160

     AAG CCG AGG CGG TGA GCCGGGCA GGAGGAAGGA GCCTCCCTCA
     K   P   R   R   O
             +165

661  GGGTTTCGGG AACCAGATCT CTCACCAGGA AAGACTGATA CAGAACGATC

     GATACAGAAA CCACGCTGCC GCCACCACAC CATCACCATC GACAGAACAG

761  TCCTTAATCC AGAAACCTGA AATGAAGGAA GAGGAGACTC TGCGCAGAGC

     ACTTTGGGTC CGGAGGGCGA GACTCCGGCG GAAGCATTCC CGGGCGGGTG

861  ACCCAGCACG GTCCCTCTTG GAATTGGATT CGCCATTTTA TTTTTCTTGC

     TGCTAAATCA CGGAGCCCGG AAGATTAGAG AGTTTTATTT CTGGGATTCC

961  TGTAGACACA CCGCGGCCGC CAGCACACTG
```

FIG. 1B

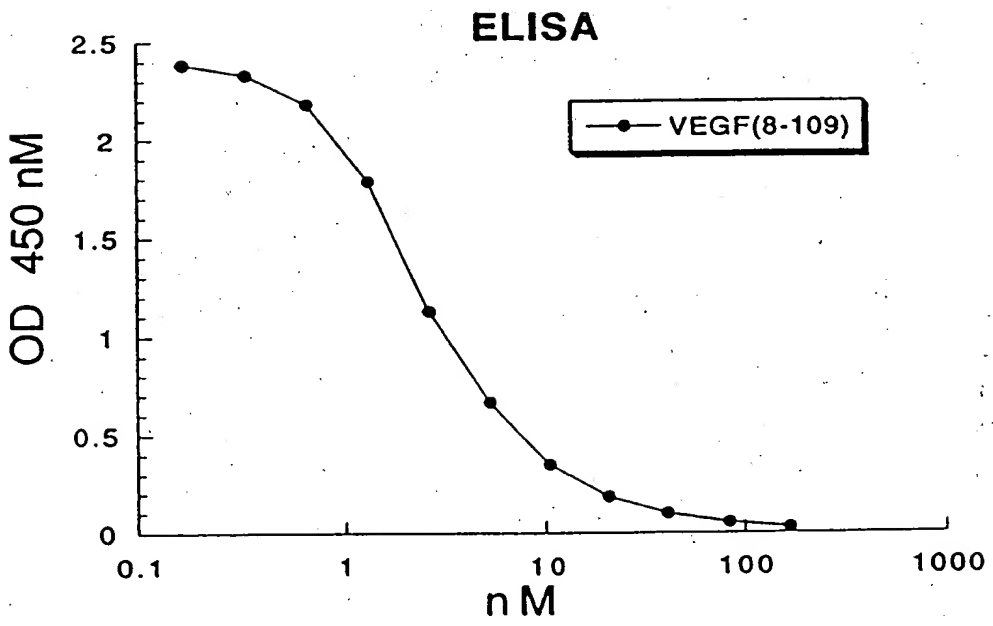


Fig. 2

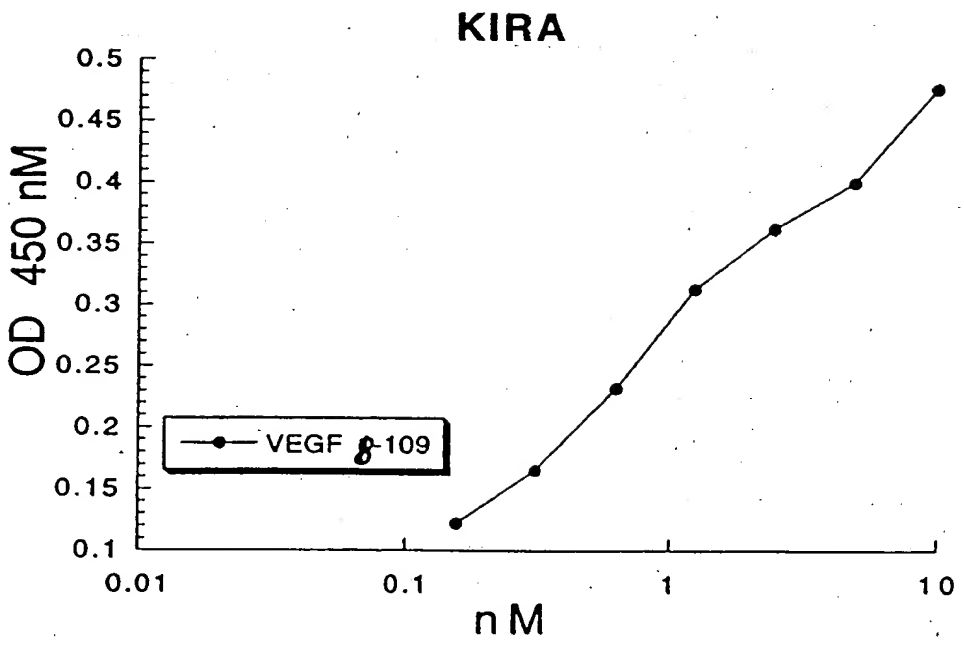

KIRA
OD 450 nM
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
VEGF 8-109
0.01
0.1
1
10
nM

Fig. 3

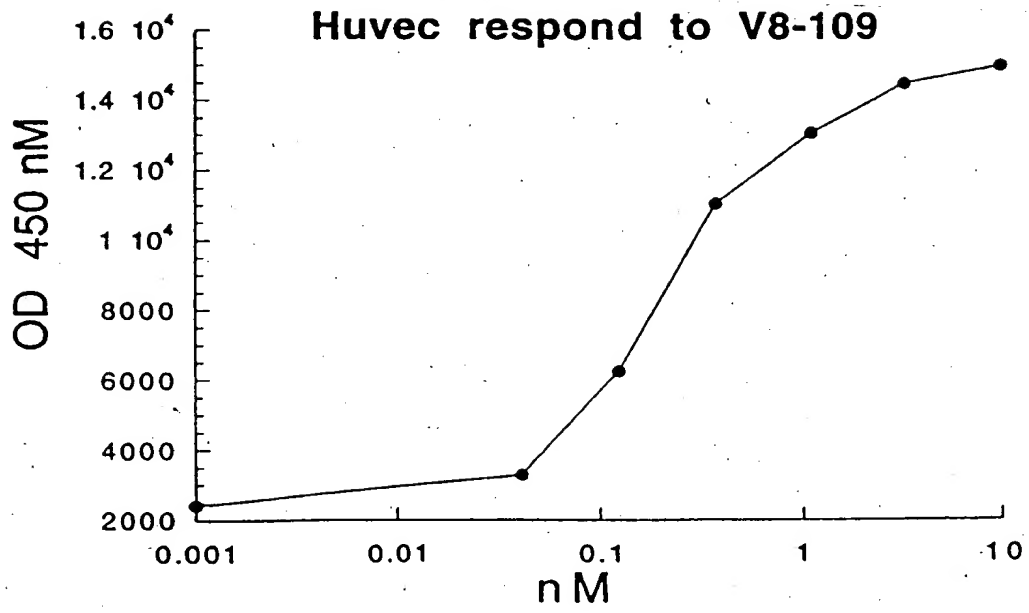

Huvec respond to V8-109
OD 450 nM
1.6 10⁴
1.4 10⁴
1.2 10⁴
1 10⁴
8000
6000
4000
2000
0.001
0.01
0.1
1
10
nM

Fig. 4

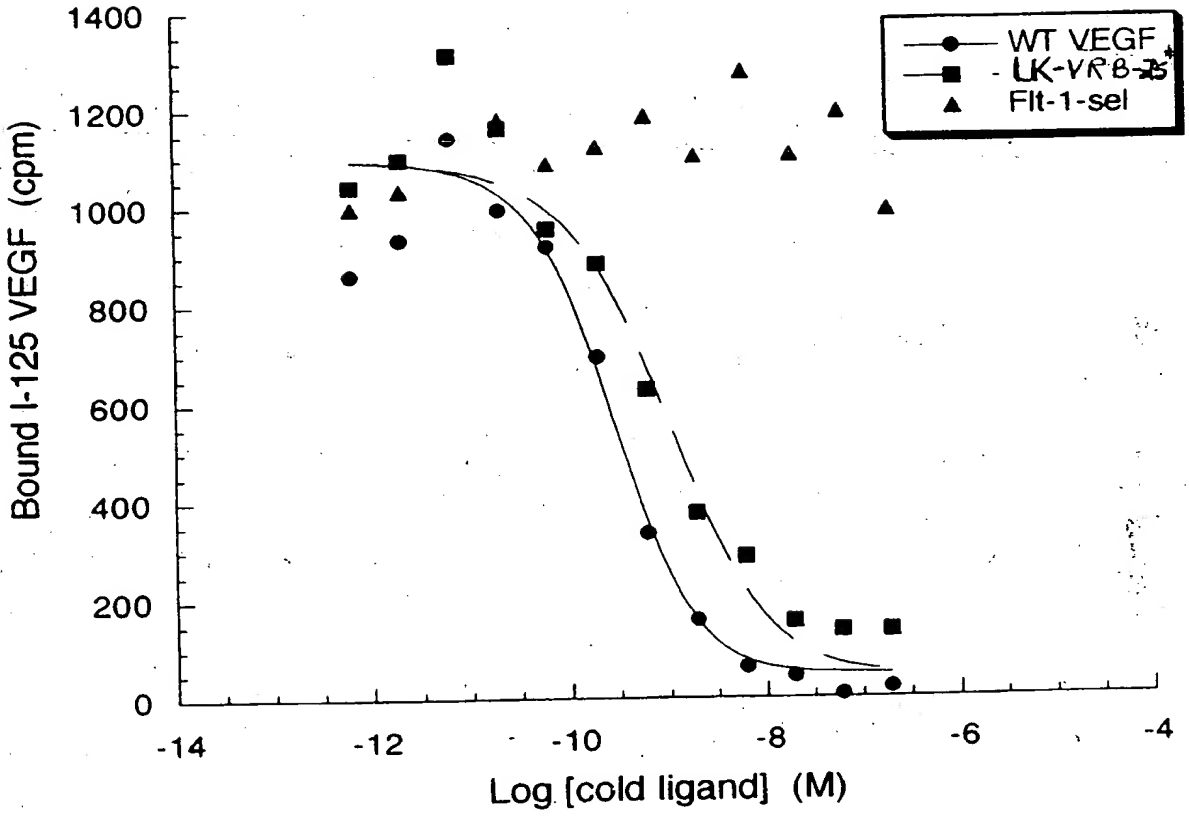

1400
1200
1000
800
600
400
200
0
Bound I-125 VEGF (cpm)
-14
-12
-10
-8
-6
-4
Log [cold ligand] (M)
WT VEGF
LK-VR8-25
Flt-1-sel

Fig. 5

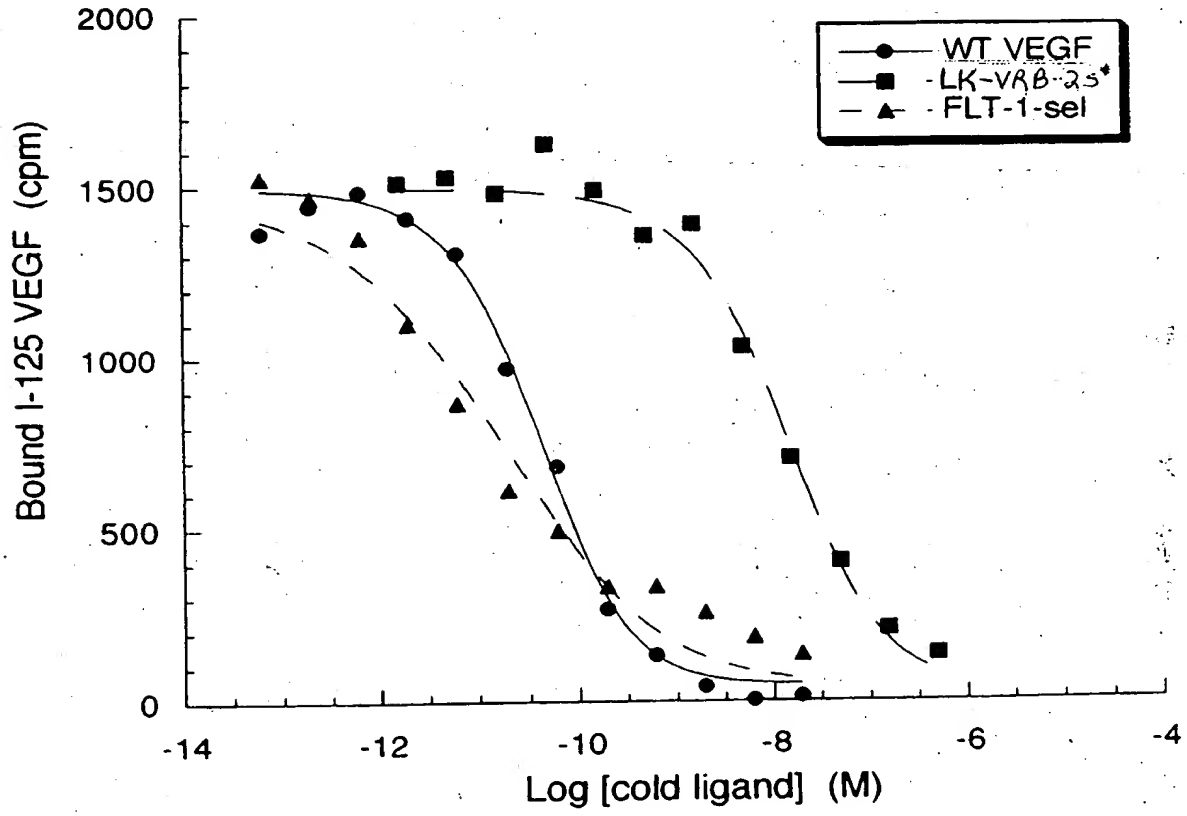

2000
1500
1000
500
0
Bound I-125 VEGF (cpm)
-14
-12
-10
-8
-6
-4
Log [cold ligand] (M)
WT VEGF
LK-VRB-2s*
FLT-1-sel

Fig. 6

Fold reduction in binding f VEGF alanine mutants

Residue	KDR(1-3)	Flt(1-3)
VEGF(1-109)	1 (10 nM)	1 (6 nM)
20s helix:		
Lys 16	1	1
Phe 17*	45	34
Met 18**	5	9
Tyr 21**	19	29
Gln 22**	6	15
Tyr 25**	6	7
40s loop:		
Ile 43*	21	3
Ile 46*	96	4
Phe 47**	5	3
Lys 48**	1	1
60s loop:		
Asp 63**	1	8
Glu 64*	10	5
Gly 65**	1	1
Leu 66**	1	10
80s loop:		
Gln 79*	55	3
Met 81**	9	5
Ile 83*	89	7
His 86**	2	1
Gln 89	1	1
Ile 91	1	1
100s loop:		
Lys 101	1	1
Glu 103	1	1
Arg 105	1	1
Pro 106	1	1

Fig. 7

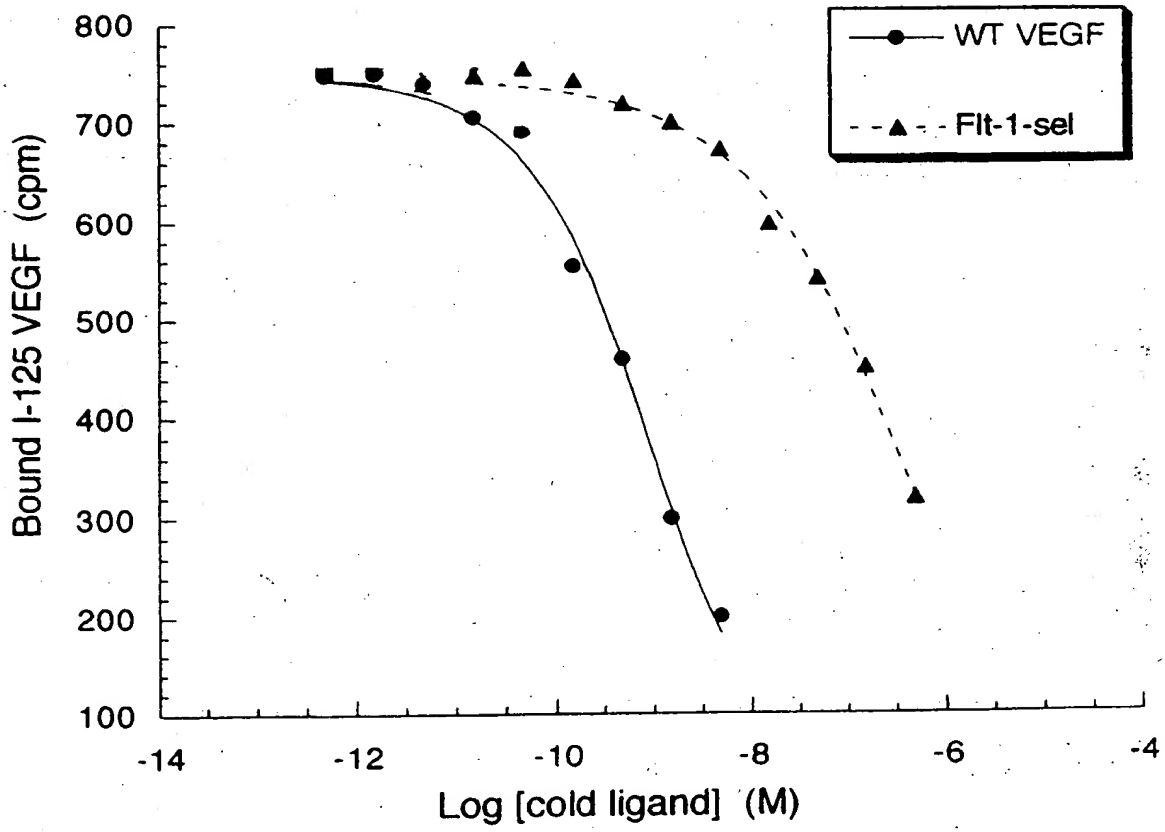

800
700
600
500
400
300
200
100
Bound I-125 VEGF (cpm)
-14
-12
-10
-8
-6
-4
Log [cold ligand] (M)
WT VEGF
Flt-1-sel

Fig. 8A

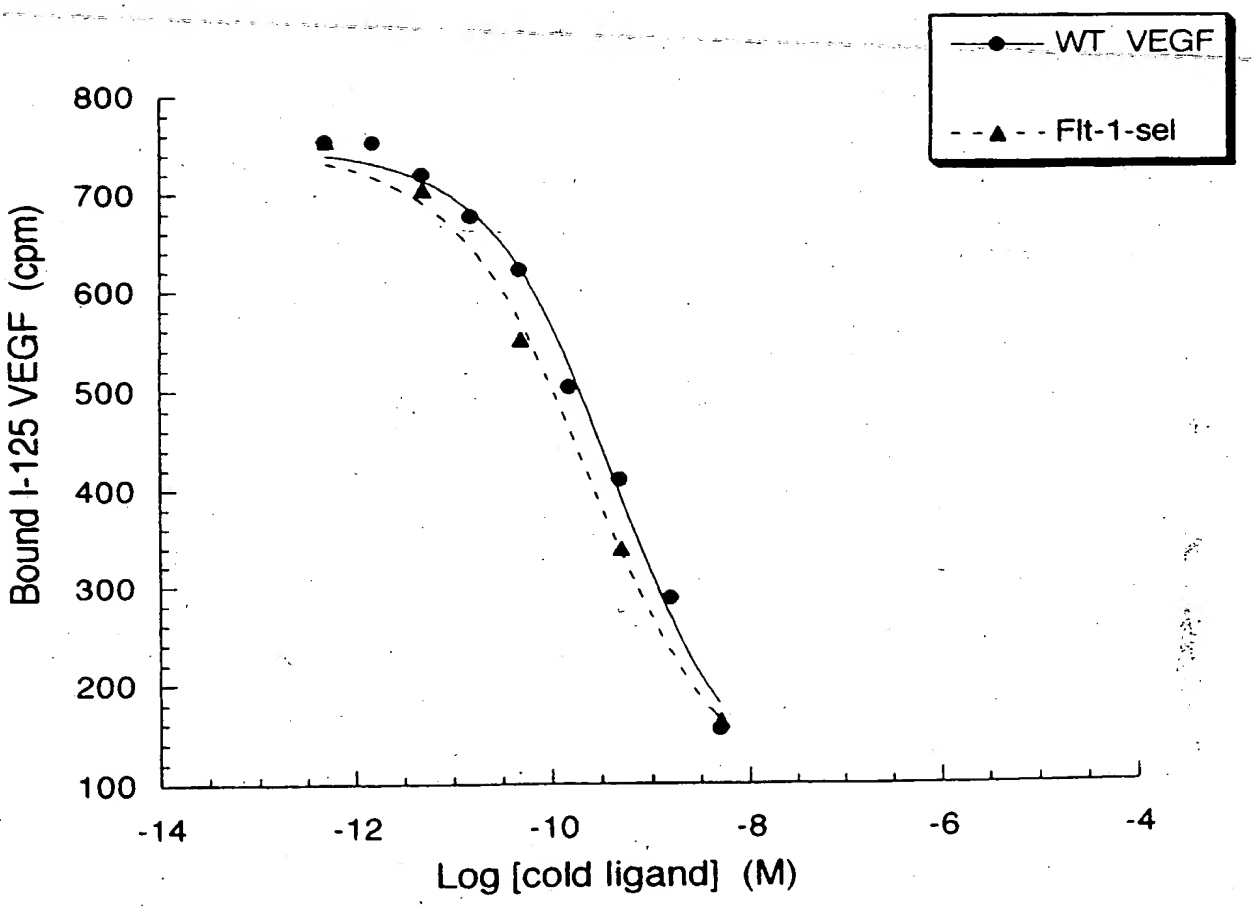

WT VEGF
Flt-1-sel
Bound I-125 VEGF (cpm)
800
700
600
500
400
300
200
100
-14
-12
-10
-8
-6
-4
Log [cold ligand] (M)

Fig. 8B

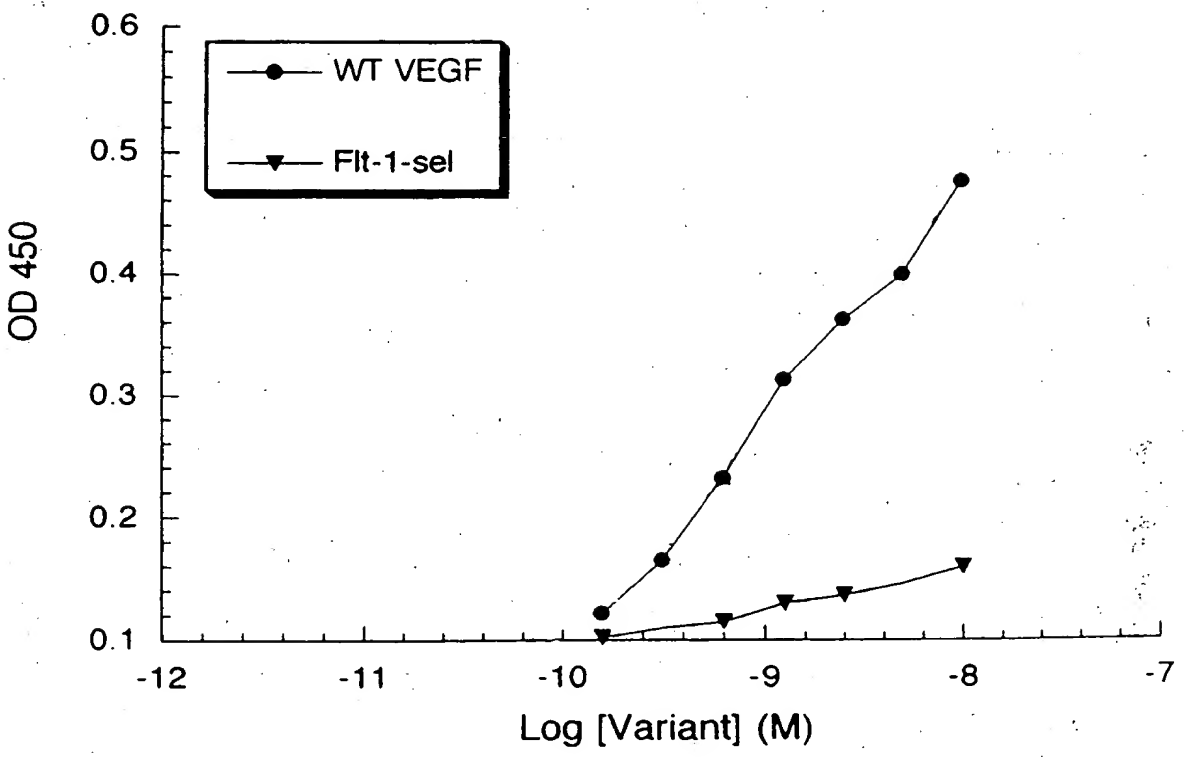

WT VEGF
Flt-1-sel
OD 450
0.6
0.5
0.4
0.3
0.2
0.1
-12
-11
-10
-9
-8
-7
Log [Variant] (M)

Fig. 9

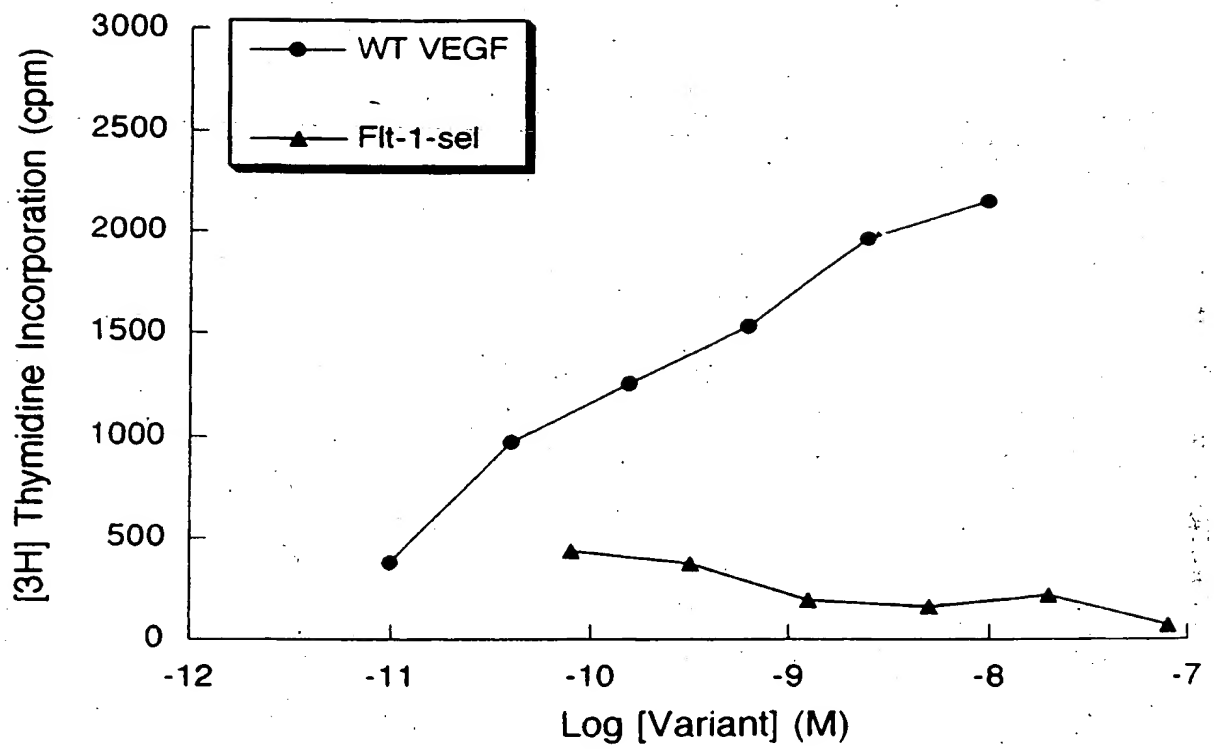

WT VEGF
Flt-1-sel
[3H] Thymidine Incorporation (cpm)
3000
2500
2000
1500
1000
500
0
-12
-11
-10
-9
-8
-7
Log [Variant] (M)

Fig. 10

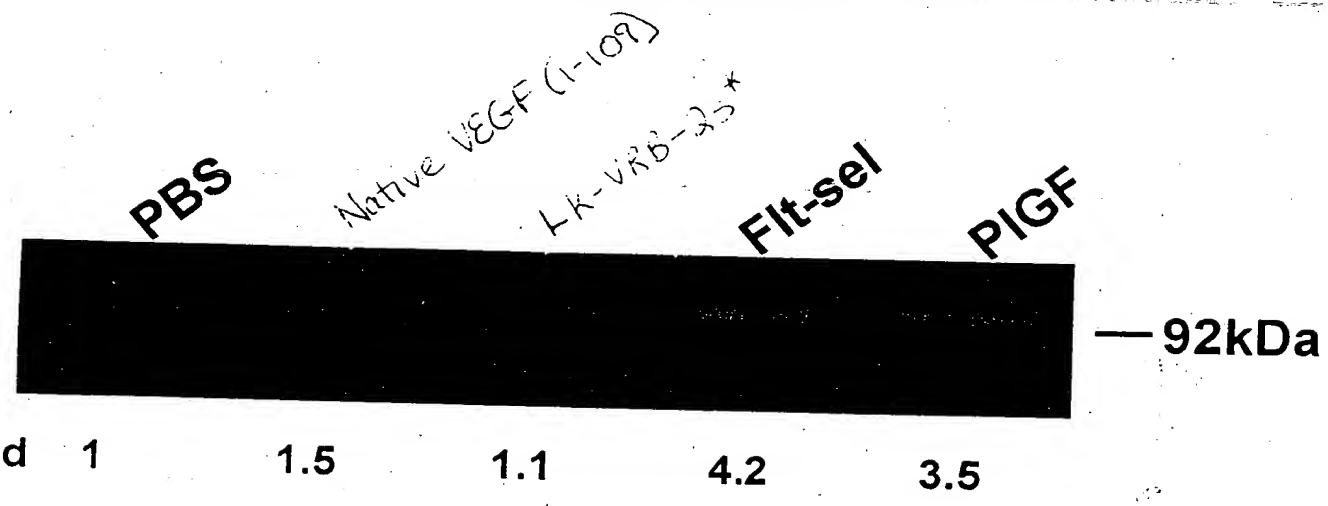

PBS
Native VEGF (1-109)
LK-VRB-35*
Flt-sel
PlGF
92kDa
Fold 1 1.5 1.1 4.2 3.5

Fig. 11

Figure 12A

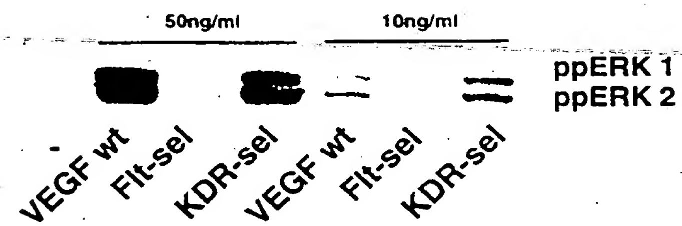


Fig. 12B

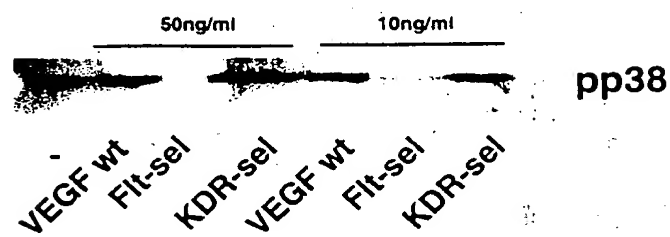


Fig. 13A

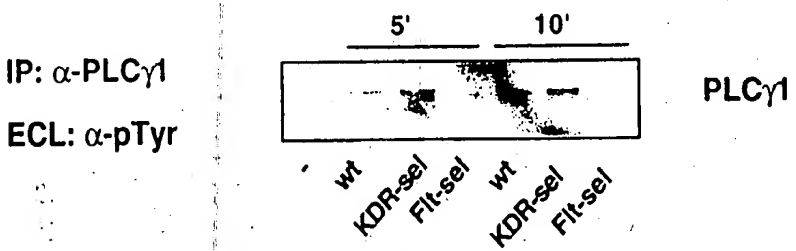


Fig. 13B

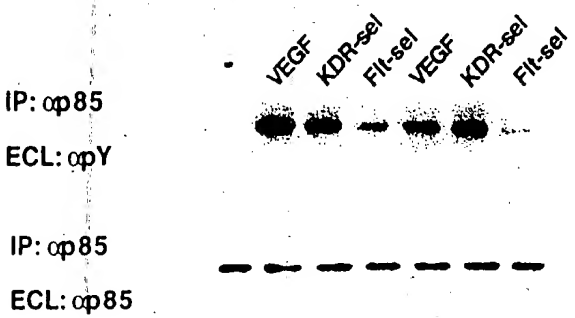


Fig. 14A

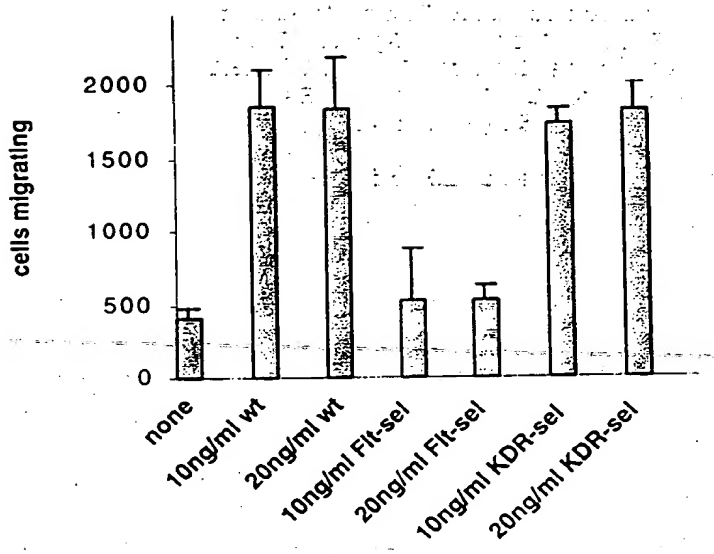


Fig. 14B

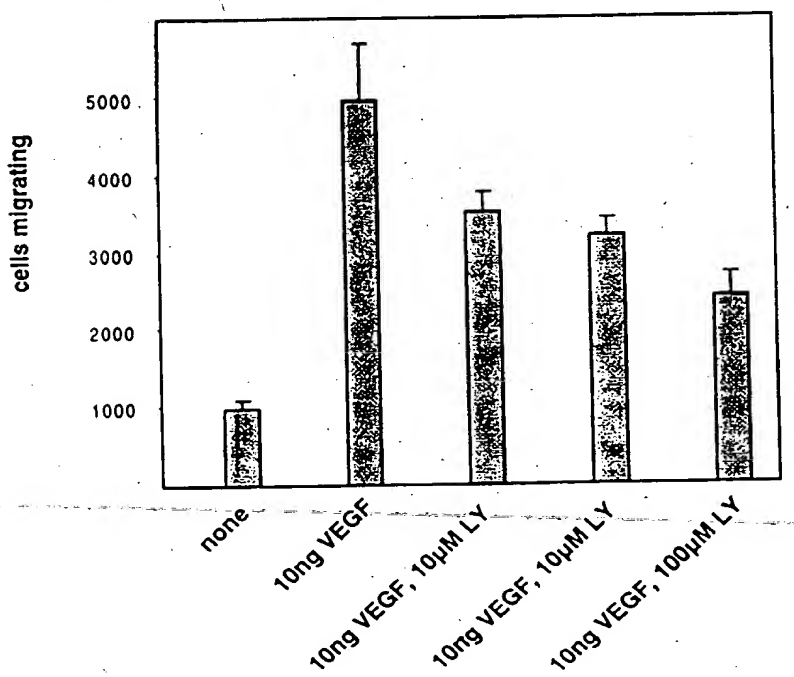
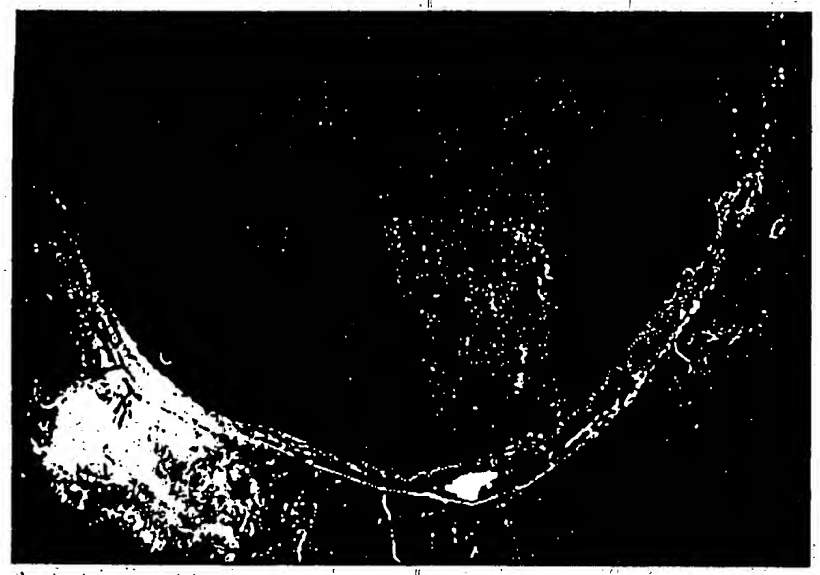
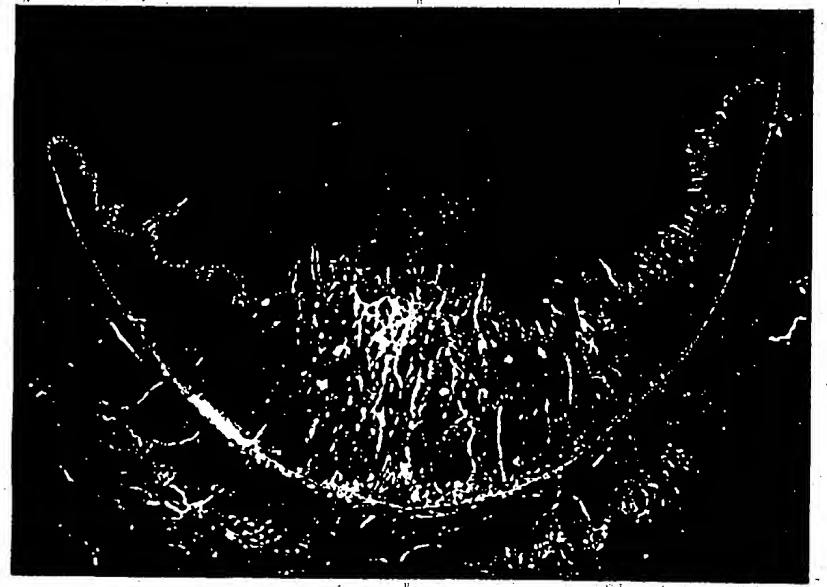


Fig. 15A

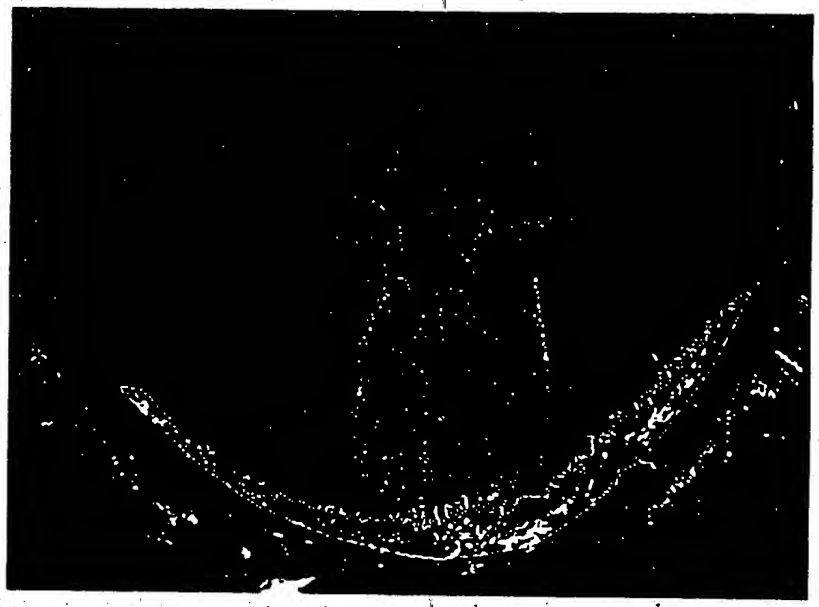


Control

VEGF



KDR-selective VEGF



Flt-selectiv VEGF

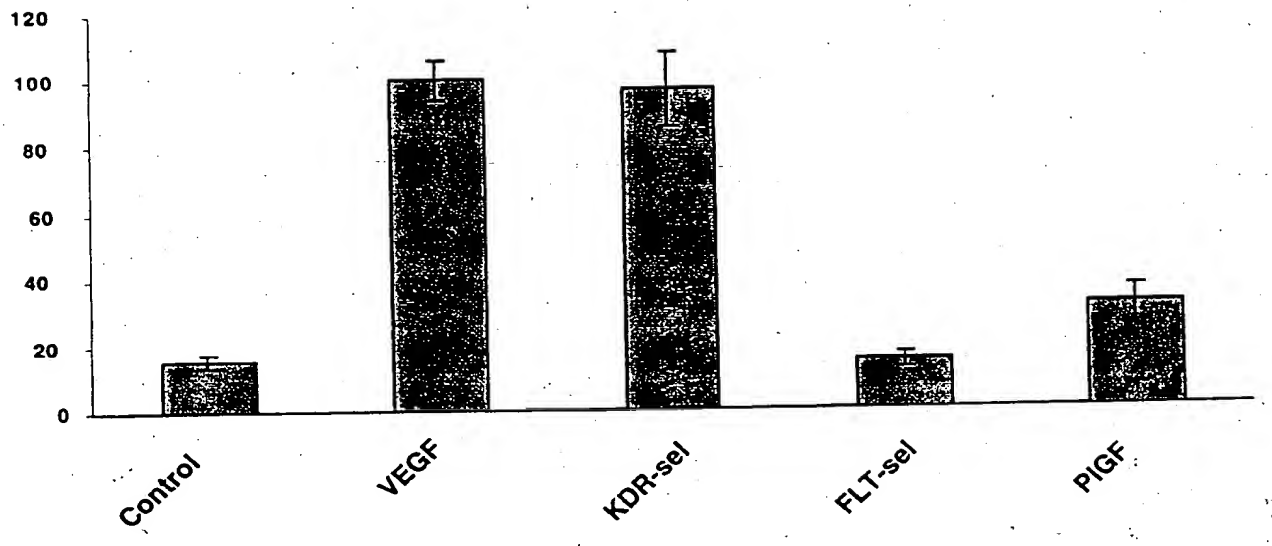


Fig. 15B